

Mitogenomic diversity in Tatars from the Volga-Ural region of Russia

Malyarchuk B., Derenko M., Denisova G., Kravtsova O.
Kazan Federal University, 420008, Kremlevskaya 18, Kazan, Russia

Abstract

To investigate diversity of mitochondrial gene pool of Tatars inhabiting the territory of the middle Volga River basin, 197 individuals from two populations representing Kazan Tatars and Mishars were subjected for analysis of mitochondrial DNA (mtDNA) control region variation. In addition, 73 mitochondrial genomes of individuals from Mishar population were sequenced completely. It was found that mitochondrial gene pool of the Volga Tatars consists of two parts, but western Eurasian component prevails considerably (84% on average) over eastern Asian one (16%). Eastern Asian mtDNAs detected in Tatars belonged to a heterogeneous set of haplogroups (A, C, D, G, M7, M10, N9a, Y, and Z), although only haplogroups A and D were revealed simultaneously in both populations. Complete mtDNA variation study revealed that the age of western Eurasian haplogroups (such as U4, HV0a, and H) is less than 18,000 years, thus suggesting re-expansion of eastern Europeans soon after the Last Glacial Maximum. © 2010 The Author.

<http://dx.doi.org/10.1093/molbev/msq065>

Keywords

genetic diversity, genome sequencing, mitochondrial DNA, Turkic-speaking populations, Volga Tatars